ABSTRACT

Methods of identifying changes in genomic DNA copy number are disclosed. Methods for identifying homozygous deletions and genetic amplifications are disclosed. An array of probes designed to detect presence or absence of a plurality of different sequences is also disclosed. The probes are designed to hybridize to sequences that are predicted to be present in a reduced complexity sample. The methods may be used to detect copy number changes in cancerous tissue compared to normal tissue. The methods may be used to diagnose cancer and other diseases associated with chromosomal anomalies.